Pseudogenes are ideal markers of genome remodelling. In turn, the mouse is an ideal platform for studying them, particularly with the availability of transcriptional time course data during development (just completed in phase 3 of ENCODE) and the sequencing of 18 strains (completed by the Mouse Genome Project). Here we present a comprehensive genome-wide annotation of the pseudogenes in the mouse reference genome and associated strains. We compiled this by combining manual curation of over 10,000 pseudogenes with results from automatic annotation pipelines. Also, by comparing human and mouse, we annotated 217 new unitary pseudogenes in human and 237 unitary pseudogenes in mouse. (We make our annotation available through a resource website mouse.pseudogene.org.) The overall mouse pseudogene repertoire (in the reference and strains) is similar to human in terms of overall size, biotype distribution (~80% processed, 20% duplicated) and top family composition (with many GAPDH and ribosomal pseudogenes). However, notable differences arise in the age distribution of pseudogenes with multiple retro-transpositional bursts in mouse evolutionary history and only a single one in human. Furthermore, in each strain ~20% of the pseudogenes are unique, reflecting strain-specific functions and evolution – e.g. the pseudogenization of taste receptors can be linked to a change in the diet. Additionally we show that processed pseudogenes are commonly associated with highly transcribed genes. Finally, we find that ~15% of the pseudogenes are transcribed, a fraction similar to human, and that pseudogenes exhibit greater tissue and strain specificity compared to their protein coding counterparts.